This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS

1 to 28 (Cancelled)

29. *(new)* A process for producing ethanol, comprising the steps of:

(a) fermenting medium containing a source of xylose with a cultured eukaryotic cell that

(i) is transformed with a nucleic acid expression construct comprising a nucleotide sequence that encodes xylose isomerase protein, the amino acid sequence of which:

(A) is at least 95% identical with SEQ ID NO:1,

(B) comprises a first xylose isomerase signature pattern;

(C) comprises a second xylose isomerase signature pattern;

(D) comprises a catalytic triad including the following four residues at the indicated positions in SEQ ID NO:1:

His 102 plus Asp 105, and Asp 340 and Lys 235;

(E) comprises at least one Mg-binding site that is residue Glu 233 of SEQ ID NO:1; and

(ii) operative linked to the nucleotide sequence of (i), a promoter that drives active expression of the xylose isomerase coding sequence in the transformed cell,

wherein the expression construct is expressible in said cell, and expression thereof confers on the cell the ability to directly isomerize xylose to xylulose, and thereby, to produce ethanol; and

(b) optionally, recovering the ethanol from said medium.

30. *(new)* The process according to claim 29 wherein the cell is a yeast cell.

31. *(new)* The process according to claim 29, wherein the medium also contains a source of glucose.

32. *(new)* The process according to claim 29, wherein the production of ethanol occurs at a rate of at least 0.5 g ethanol per liter per hour.

33. *(new)* The process according to claim 29, wherein the ethanol yield is at least 50%.

34. *(new)* A process for producing a non-ethanolic fermentation product fermentation product, which process comprises the steps of:

(a) fermenting a medium containing a source of xylose with a cultured eukaryotic cell that:

(i) is transformed with a nucleic acid expression construct comprising a nucleotide sequence that encodes xylose isomerase protein, the amino acid sequence of which

(A) is at least 95% identical with SEQ ID NO:1,

(B) comprises a first xylose isomerase signature pattern;

(C) comprises a second xylose isomerase signature pattern;

(D) comprises a catalytic triad including the following four residues at the indicated positions in SEQ ID NO:1:

His 102 plus Asp 105, and Asp 340 and Lys 235;

(E) comprises at least one Mg-binding site that is residue Glu 233 of SEQ ID NO:1; and

which nucleotide sequence is operative linked to a promoter that drives active expression of the xylose isomerase coding sequence in the transformed cell,

(ii) expresses one or more enzymes that confers on the cell the ability to produce a non-ethanolic fermentation product,

wherein, expression of the construct confers on the cell the ability to directly ferment and isomerize xylose to xylulose and thereby produce said non-ethanolic fermentation product; and

(b) optionally, recovering the non-ethanolic fermentation product from said medium.

35. *(new)* The process of claim 34 wherein the fermentation product is selected from the group consisting of lactic acid, acetic acid, succinic acid, an amino acid, 1,3-propanediol, ethylene, and glycerol.

36. *(new)* The process of claim 34 wherein the fermentation product is a β-lactam antibiotic or a cephalosporin.

37. *(new)* A process according to claim 34, wherein the medium also contains a source of glucose.

38. *(new)* The process of claim 34, wherein the cell further comprises a genetic modification that results in decreased alcohol dehydrogenase activity so as to reduce ethanol production by said cell.

39. *(new))*: A cultured eukaryotic cell transformed with a nucleic acid expression construct which construct comprises:

(a) a nucleotide sequence that encodes xylose isomerase protein, the amino acid sequence of which

(i) is at least 95% identical with SEQ ID NO:1,

(ii) comprises a first xylose isomerase signature pattern;

(iii) comprises a second xylose isomerase signature pattern;

(iv) comprises a catalytic triad including the following four residues at the indicated positions in SEQ ID NO:1: His 102 plus Asp 105, and Asp 340 and Lys 235;

(v) comprises at least one Mg-binding site that is residue Glu 233 of SEQ ID NO:1; and

(b) operative linked to the nucleotide sequence of (i), a promoter that drives active expression of the xylose isomerase coding sequence in the transformed cell,

wherein, said expression construct is expressible in said cell and expression thereof confers on the cell the ability to directly isomerize xylose to xylulose.

40. *(new)* The cell according to claim 39, wherein the nucleotide sequence encodes a xylose isomerase the amino acid sequence of which is SEQ ID NO:1.

41. *(new/mildly amended)*: The cell according to claim 39, wherein the cell is a yeast cell.

42. *(new)* The yeast cell of claim 44 that is a member of a genus selected from the group consisting of *Saccharomyces*, *Kluyveromyces*, *Candida*, *Pichia, Schizosaccharomyces*, *Hansenula*, *Kloeckera*, *Schwanniomyces*, and *Yarrowia.*

43. *(new)* The yeast cell according to claim 45 that is a member of a species selected from the group consisting of *S. cerevisiae*, *S. bulderi*, *S. barnetti*, *S. exiguus*, *S. uvarum*, *S. diastaticus*, *K. lactis, K. marxianus*, and *K. fragilis*.

44. *(new)*: The cell according to claim 39, wherein the cell is a filamentous fungus.

45. *(new)* The filamentous fungus cell of claim 44 that is a member of a genus selected from the group consisting of *Aspergillus*, *Trichoderma*, *Humicola*, *Acremonium*, *Fusarium*, and *Penicillium*.

46. *(new)* The cell according to claim 39, wherein the promoter is insensitive to catabolite repression in the cell.

47. *(new)* The cell according to claim 39 that has been further genetically modified to confer on the cell one or more of the following properties:

(1) increased transport of xylose into the host cell;
(2) increased xylulose kinase activity;
(3) increased flux of the pentose phosphate pathway;
(4) decreased sensitivity to catabolite repression;
(5) increased tolerance to ethanol, osmolarity or organic acids; or
(6) decreased production of by-products,

in comparison to a similar cell that has not undergone said genetic modification..

48. *(new)* The cell according to claim 47, wherein the nucleotide sequence encodes a xylose isomerase the amino acid sequence of which is SEQ ID NO:1.

49. *(new)* The cell according to claim 47, wherein the genetic modification that results in said properties (1) – (6) is

(A) overexpression of an endogenous gene,
(B) expression of a heterologous gene, or
    (ii) a pentose transporter;
    (iii) a xylulose kinase;
    (iv) an enzyme from the pentose phosphate pathway,
    (v) a glycolytic enzyme, or
    (vi) an ethanologenic enzyme.

50. *(new)* The cell according to claim 47 wherein the genetic modification that results in said properties (1) – (6) is one that causes inactivation of one of the following endogenous genes:

(a) a gene encoding a hexose kinase

(b) *Saccharomyces MIG1* gene;

(c) *Saccharomyces MIG2* gene; or

(d) a gene homologous to (a), (b) or (c) and which hybridizes thereto.

51. *(new)* The cell according to claim 39, that further expresses one or more enzymes that confers on the cell the ability to produce a non-ethanolic fermentation product.

52 *(new)* The cell according to claims 51 which is a yeast cell.

53 *(new)* The cell according to claim 52 wherein said fermentation product is selected from the group consisting of lactic acid, acetic acid, succinic acid, amino acids, 1,3-propanediol, ethylene, and glycerol.

54. *(new)* The cell according to claim 51, wherein the cell is a filamentous fungus.

55 *(new)* The cell according to claim 51 wherein said fermentation product is a β-lactam antibiotic or a cephalosporin.

56. *(new)* The cell according to claim 52 in which alcohol dehydrogenase activity is genetically decreased so as to reduce ethanol production by said cell.